Amendments to the Claims

The listing of claims set forth below will replace all prior versions and listings of claims in the application.

1-17 (Cancelled)

18. (Currently Amended) A process for preparing a cell capable of stable ~~high yield~~ expression of a target gene product having an essentially human glycosylation pattern, wherein the target gene product is a secreted protein, which method comprises:

(a) selecting an immortalized human cell or human hybrid cell (starting cell) which is derived from B lymphocytes and is capable of stable ~~high yield~~ expression of an immunoglobulin (Ig) being non-essential to the starting cell;

(b) ~~screening for the locus of the Ig gene within the genome of the starting cell;~~

~~(c)~~ replacing ~~the~~ a gene coding for the Ig with a first functional DNA sequence containing one or more recombinase recognition sites (RRS) to obtain a functionalized precursor cell; and

~~(d)~~(c) administering a recombinase recognizing the RRSs incorporated with the first functional sequence and ~~integrating~~ a second functional DNA sequence containing a DNA sequence coding for the target gene product, wherein the second functional DNA sequence is integrated into the functionalized precursor cell obtained in step (b)~~(c) by use of a recombinase recognizing the RRSs incorporated with the first functional sequence~~, or

~~(e)~~(d) directly replacing the gene coding for the Ig with a functional DNA sequence containing a DNA sequence coding for the target gene product.

19. (Previously Presented) The method of claim 18, wherein the starting cell secretes the Ig in an amount of at least 0.3 fmol/cell/d of a polypeptide chain.

20. (Previously Presented) The method of claim 19, wherein the starting cell secretes the Ig in an amount of more than 1 fmol/cell/d of a polypeptide chain.

21. (Previously Presented) The method of claim 18, wherein the starting cell is a human hybrid cell and the Ig gene is a human gene.

22. (Previously Presented) The method of claim 18 wherein the starting cell is selected from the group consisting of a human myeloma, a human hybridoma, and a human hetero-hybridoma cell.

23. (Previously Presented) The method of claim 22, where the starting cell is human-mouse hetero-hybridoma H-CB-P1 (DSM ACC2104).

24. (Previously Presented) The method of claim 18, wherein the integration of the functional DNA sequence(s) is effected at a rearranged Ig locus of said starting cell.

25. (Previously Presented) The method of claim 24, where the integration of the functional DNA sequence(s) is effected at a rearranged immunoglobulin H locus of said starting cell.

26. (Previously Presented) The method of claim 24, where the integration of the functional DNA sequence(s) is effected at a locus of said starting cell.

27. (Canceled)

28. (Previously Presented) The method of claim 18, wherein the locus of the Ig gene is determined by a screening procedure selected from the group consisting of microarray expression analysis, 2D protein gel electrophoresis, quantitative PCR, RNAse protection, northern blot, ELISA, western blot and combinations thereof.

29. (Previously Presented) The method of claim 27 wherein the locus of the Ig gene is selected as to provide for an essentially human glycosylation pattern.

30. (Previously Presented) The method of claim 18, wherein the replacement of the Ig gene is effected by an one step replacement strategy, wherein the starting cell is contacted with a vector construct containing the first functional sequence, said first functional sequence replacing the gene coding for the Ig.

31. (Previously Presented) The method of claim 18, wherein the replacement of the Ig gene is effected in a two- or multi-step strategy, wherein the gene coding for the Ig gene is deleted or inactivated and subsequently contacted with a vector construct containing the first functional sequence, said first functional sequence being incorporated at the site of the deleted/inactivated Ig.

32. (Previously Presented) The method of claim 18, wherein the first functional DNA sequence comprises one or more RRS(s) selected from the group consisting of loxP, frt, attL and attR sites of lambdoid phages, and recognition sites for resolvases or phage C31 integrase.

33. (Currently Amended) The method of claim 32 wherein the RRS(s) are capable of unidirectional integration.

34. (Previously Presented) The method of claim 32 wherein the RRS(s) are selected from the group consisting of modified loxP sites and frt sites.

35. (Previously Presented) The method of claim 18, wherein the first functional DNA sequence further comprises functional sequences selected from the group consisting of marker sequences, secretion proteins, promoters, enhancers, splice signals, polyadenylation signals and IRES elements.

36. (Previously Presented) The method of claim 18, wherein the first functional DNA sequence is flanked in the vector by sequences selected for the group consisting of sequences that are homologous to the target gene or adjacent sequences.

37. (Previously Presented) The method of claim 18, wherein the integration of the second functional DNA sequence is effected by delivering a recombinases recognizing the RRS(s) present in the first functional sequence together with, shortly before or after delivery of the second functional sequence.

38. (Currently Amended) The method of claim 18, wherein the integrase is selected from the group ~~consistin~~ consisting of Cre, Flp, C31 integrase and resolvase.

39. (Previously Presented) The method of claim 18, wherein the target gene product is selected from the group consisting of enzymes, hormones, cytokines, receptors, antibodies, antibody domains and fusion proteins comprising the gene product mentioned before.

40. (Previously Presented) The method of claim 18, wherein the second functional DNA sequence further comprises functional sequences selected from the group consisting of promoter sequences, marker sequences, splice donor and acceptor sequences and

recombinase recognition sequences differing from the RRS of the first functional sequence.

41. (Previously Presented) The method of claim 18, wherein the gene coding for the Ig is directly replaced with a functional DNA sequence containing a DNA sequence coding for the target gene product.

42. (Currently Amended) A method for preparing a functionalized cell comprising the steps

(a) selecting an immortalized human cell or human hybrid cell (starting cell) which is derived from B lymphocytes and is capable of stable high yield expression of an immunoglobulin (Ig) being non-essential to the starting cell;

(b) ~~screening for the locus of the Ig gene within the genome of the starting cell;~~

~~(c)~~ replacing ~~the~~ a gene coding for the Ig with a first functional DNA sequence containing one or more recombinase recognition sites (RRS) to obtain a functionalized precursor cell.

43. (Previously Presented) A functionalized cell as obtainable by the method of claim 25.

44. (Previously Presented) The functionalized cell of claim 43, which is derived from H-CB-P1 (DSM ACC2104).

45. (Currently Amended) A cell capable of ~~high yield~~ expression of a target gene product obtainable by the method of claim 18.

46. (Previously Presented) The cell of claim 45, which is derived from H-CB-P1 (DSM ACC2104).

47. (Previously Presented) The cell of claim 45, wherein the target gene product is an antibody.

48. (Currently Amended) The cell of claim 47, wherein the cell is PBG04 (~~DMS~~ DSM ACC2577).

49. (Previously Presented) The cell of claim 47, which is derived from H-CB-P1 (DSM ACC2104).

50. (Currently Amended) The cell of claim 47, wherein the gene sequence encoding the light chain of the antibody ~~further having its light chain~~ has been inactivated or replaced with a gene coding for the same or a different target gene product.

51. (Currently Amended) A method for producing a secreted ~~high yield expression of a~~ target gene product which comprises cultivating a cell as defined in claim 45.

52. (Withdrawn) A target gene product obtained by cultivating a cell as defined in claim 42.

53. (Withdrawn) A target gene product obtained by cultivating a cell as defined in claim 45.